

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/008,960DATE: 12/10/2002
TIME: 10:27:50

INPUT SET: S36943.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

- (i) APPLICANT: BAYLOR COLLEGE OF MEDICINE
SMITH, JAMES R.
DRUTZ, DAVID J.
WILSON, DEBORAH R.
ZUMSTEIN, LOUIS A.

- (ii) TITLE OF INVENTION: SENESCENT CELL DERIVED INHIBITORS OF
DNA SYNTHESIS

- (iii) NUMBER OF SEQUENCES: 36

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: ROGERS & WELLS
(B) STREET: 200 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10166

ENTERED

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 10/008,960
(B) FILING DATE: 07-DEC-2001
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08 327,874
(B) FILING DATE:

(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/808,523
(B) FILING DATE: 16-DEC-1991

(ix) PRIOR APPLICATION DATA:

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47 (A) APPLICATION NUMBER: US 07/970,462
48 (B) FILING DATE: 02-NOV-1992
49
50 (vii) PRIOR APPLICATION DATA:
51 (A) APPLICATION NUMBER: US 08/113,372
52 (B) FILING DATE: 30-AUG-1993
53
54 (vii) PRIOR APPLICATION DATA:
55 (A) APPLICATION NUMBER: US 08/153,564
56 (B) FILING DATE: 17-NOV-1993
57
58 (vii) PRIOR APPLICATION DATA:
59 (A) APPLICATION NUMBER: US 08/203,535
60 (B) FILING DATE: 25-FEB-1994
61
62 (vii) PRIOR APPLICATION DATA:
63 (A) APPLICATION NUMBER: US 08/229,420
64 (B) FILING DATE: 15-APR-1994
65
66 (vii) PRIOR APPLICATION DATA:
67 (A) APPLICATION NUMBER: US 08/274,535
68 (B) FILING DATE: 13-JUL-1994
69
70 (vii) PRIOR APPLICATION DATA:
71 (A) APPLICATION NUMBER: PCT US94/09700
72 (B) FILING DATE: 26-AUG-1994
73
74 (vii) PRIOR APPLICATION DATA:
75 (A) APPLICATION NUMBER: 08/327,874
76 (B) FILING DATE: 24-OCT-1994
77
78 (viii) ATTORNEY/AGENT INFORMATION:
79 (A) NAME: NORTON, GERARD P.
80 (B) REGISTRATION NUMBER: 36,621
81 (C) REFERENCE/DOCKET NUMBER: 3634-8-CIP10
82
83 (ix) TELECOMMUNICATION INFORMATION:
84 (A) TELEPHONE: (212) 878-3148
85 (B) TELEFAX: (212) 878-8375
86
87 (2) INFORMATION FOR SEQ ID NO:1:
88
89 (i) SEQUENCE CHARACTERISTICS:
90 (A) LENGTH: 2106 base pairs
91 (B) TYPE: nucleic acid
92 (C) STRANDEDNESS: single
93 (D) TOPOLOGY: linear
94
95 (ii) MOLECULE TYPE: cDNA
96
97 (iii) HYPOTHETICAL: NO
98
99 (iv) ANTI-SENSE: NO

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100
101 (vi) ORIGINAL SOURCE:
102 (A) ORGANISM: Homo sapiens
103 (G) CELL TYPE: SENESCENT HUMAN CELLS
104
105 (vii) IMMEDIATE SOURCE:
106 (A) LIBRARY: SENESCENT CELL DERIVED CDNA LIBRARY
107 (B) CLONE: SDI-1
108
109 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
110
111 CCTGCCGAAG TCAGTTCCTT GTGGAGCCGG AGCTGGGCGC GGATTTCGCCG AGGCACCGAG 60
112 GCACTCAGAG GAGGCGCCAT GTCAGAACCG GCTGGGGATG TCCGTCAGAA CCCATGCGGC 120
113 AGCAAGGCCT GCCGCCGCCT CTTCCGCCCA GTGGACAGCG AGCAGCTGAG CCGCGACTGT 180
114 GATGCGCTAA TGGCGGGCTG CATCCAGGAG GCCCGTGAGC GATGGAACCT CGACTTTGTC 240
115 ACCGAGACAC CACTGGAGGG TGACTTCGCC TGGGAGCGTG TCGGGGGCCT TGGCCTGCC 300
116 AAGCTCTACC TTCCCACGGG GCCCCGGCGA GGCCGGGATG AGTTGGGAGG AGGCAGGCGG 360
117 CCTGGCACCT CACCTGCTCT GCTGCAGGGG ACAGCAGAGG AAGACCATGT GGACCTGTCA 420
118 CTGTCTTGTA CCCTTGTCCT TCGCTCAGGG GAGCAGGCTG AAGGGTCCCC AGGTGGACCT 480
119 GGAGACTCTC AGGGTCGAAA ACGGCGGCAG ACCAGCATGA CAGATTTCTA CCACTCCAAA 540
120 CGCCGGCTGA TCTTCTCCAA GAGGAAGCCC TAATCCGCCC ACAGGAAGCC TGCAGTCCTG 600
121 GAAGCGCGAG GGCCTCAAAG GCCCGCTCTA CATCTTCTGC CTTAGTCTCA GTTTGTGTGT 660
122 CTTAATTATT ATTTGTGTTT TAATTTAAAC ACCTCCTCAT GTACATACCC TGGCCGCCCC 720
123 CTGCCCCCA GCCTCTGGCA TTAGAAATAT TTAACAAAA ACTAGGCGGT TGAATGAGAG 780
124 GTTCCTAAGA GTGCTGGGCA TTTTATTTT ATGAAATACT ATTTAAAGCC TCCTCATCCC 840
125 GTGTTCTCCT TTTCTCTCT CCCGGAGGTT GGGTGGGCCG GCTTCATGCC AGCTACTTCC 900
126 TCCTCCCCAC TTGTCCGCTG GGTGGTACCC TCTGGAGGGG TGTGGCTCCT TCCCATCGCT 960
127 GTCACAGGCG GTTATGAAAT TCACCCCTT TCCTGGACAC TCAGACCTGA ATTCTTTTTC 1020
128 ATTTGAGAAG TAAACAGATG GCACTTTGAA GGGGCCTCAC CGAGTGGGGG CATCATCAAA 1080
129 AACTTTGGAG TCCCCTCACC TCCTCTAAGG TTGGGCAGGG TGACCCTGAA GTGAGCACAG 1140
130 CCTAGGGCTG AGCTGGGGAC CTGGTACCCT CCTGGCTCTT GATACCCCCC TCTGTCTTGT 1200
131 GAAGGCAGG GGAAGGTGGG GTCTTGAGC AGACCACCCC GCCTGCCCTC ATGGCCCCCTC 1260
132 TGACCTGCAC TGGGGAGCCC GTCTCAGTGT TGAGCCTTTT CCCTCTTTGG CCCCCCTGTA 1320
133 CCTTTTGAGG AGCCCCAGCT ACCCTTCTTC TCCAGCTGGG CTCTGCAATT CCCCTCTGCT 1380
134 GCTGTCCCTC CCCCTTGTC TTTCCCTTCA GTACCCCTC AGCTCCAGGT GGCTCTGAGG 1440
135 TGCTGTCCC ACCCCACCC CCAGCTCAAT GGACTGGAAG GGAAGGGAC ACACAAGAAG 1500
136 AAGGGCACCC TAGTTCTACC TCAGGCAGCT CAAGCAGCGA CCGCCCCCTC CTCTAGCTGT 1560
137 GGGGGTGAGG GTCCCATGTG GTGGCACAGG CCCCTTGAG TGGGGTTATC TCTGTGTTAG 1620
138 GGGTATATGA TGGGGGAGTA GATCTTTCTA GGAGGGAGAC ACTGGCCCCC CAAATCGTCC 1680
139 AGCGACCTTC CTCATCCACC CCATCCCTCC CCAGTTCATT GCACTTTGAT TAGCAGCGGA 1740
140 ACAAGGAGTC AGACATTTTA AGATGGTGGC AGTAGAGGCT ATGGACAGGG CATGCCACGT 1800
141 GGGCTCATAT GGGGCTGGGA GTAGTTGTCT TTCTGGCAC TAACGTTGAG CCCCTGGAGG 1860
142 CACTGAAGTG CTTAGTGTAC TTGGAGTATT GGGGTCTGAC CCAAAACACC TTCCAGCTCC 1920
143 TGTAACATAC TGGCCTGGAC TGTCTTCTCT CGGCTCCCCA TGTGTCTTGG TTCCCGTTTC 1980
144 TCCACCTAAG TGTAAAGCT GTGGAGGCGA GGGAGGAGC GATGACCTGT TGTGTGTCTT 2040
145 TCACAGCTCC TCCCACAATG CTGATATACA GCAGGTGCTC AATAAACGAT TCTTAGTGAA 2100
146 AAAAAA 2106
147
148 (2) INFORMATION FOR SEQ ID NO:2:
149 (i) SEQUENCE CHARACTERISTICS:
150 (A) LENGTH: 164 amino acids
151 (B) TYPE: amino acid
152 (D) TOPOLOGY: linear

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153
154 (ii) MOLECULE TYPE: protein
155
156 (iii) HYPOTHETICAL: NO
157
158 (iv) ANTI-SENSE: NO
159
160 (vi) ORIGINAL SOURCE:
161 (A) ORGANISM: HOMO SAPIENS
162 (B) STRAIN: SDI-1
163
164 (vii) IMMEDIATE SOURCE:
165 (A) LIBRARY: Senescent cell derived cDNA library
166
167 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
168
169 Met Ser Glu Pro Ala Gly Asp Val Arg Gln Asn Pro Cys Gly Ser Lys
170 1 5 10 15
171 Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser Glu Gln Leu Ser Arg
172 20 25 30
173 Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln Glu Ala Arg Glu Arg
174 35 40 45
175 Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala
176 50 55 60
177 Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys Leu Tyr Leu Pro Thr
178 65 70 75 80
179 Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Gly Arg Arg Pro Gly
180 85 90 95
181 Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu Glu Asp His Val Asp
182 100 105 110
183 Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gln Ala Glu
184 115 120 125
185 Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln
186 130 135 140
187 Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser
188 145 150 155 160
189 Lys Arg Lys Pro
190
191 (2) INFORMATION FOR SEQ ID NO:3:
192
193 (i) SEQUENCE CHARACTERISTICS:
194 (A) LENGTH: 19 base pairs
195 (B) TYPE: nucleic acid
196 (C) STRANDEDNESS: single
197 (D) TOPOLOGY: linear
198
199 (ii) MOLECULE TYPE: cDNA
200
201 (iii) HYPOTHETICAL: NO
202
203 (iv) ANTI-SENSE: YES
204
205 (vi) ORIGINAL SOURCE:

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206 (A) ORGANISM: HOMO SAPIENS

207

208 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

209

210 AGCCGGTTCT GACATGGCG

19

211

212 (2) INFORMATION FOR SEQ ID NO:4:

213

(i) SEQUENCE CHARACTERISTICS:

214

(A) LENGTH: 12 amino acids

215

(B) TYPE: amino acid

216

(D) TOPOLOGY: linear

217

218 (ii) MOLECULE TYPE: peptide

219

220 (iii) HYPOTHETICAL: NO

221

222 (v) FRAGMENT TYPE: N-terminal

223

224 (vii) IMMEDIATE SOURCE:

225

(B) CLONE: [His]6 leader peptide

226

227 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

228

Met Arg Gly Ser His His His His His His Gly Ala

229

1

5

10

230

231

232 (2) INFORMATION FOR SEQ ID NO:5:

233

234 (i) SEQUENCE CHARACTERISTICS:

235

(A) LENGTH: 699 base pairs

236

(B) TYPE: nucleic acid

237

(C) STRANDEDNESS: single

238

(D) TOPOLOGY: linear

239

240 (ii) MOLECULE TYPE: cDNA

241

242 (iii) HYPOTHETICAL: NO

243

244 (iv) ANTI-SENSE: NO

245

246 (vi) ORIGINAL SOURCE:

247

(A) ORGANISM: Schistosoma japonicum

248

249 (vii) IMMEDIATE SOURCE:

250

B. CLONE: GST

251

252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

253

254	ATGTCGCTTA TACTAGCTTA TTGCAAAATT AACCGCCTTG TGCAAGCCAC TCGACTTCTT	60
255	TTGGAATATC TTGAAGAAAA ATATGAAGAG CATTTGTATG AGCGCGATGA AGGTGATAAA	120
256	TGGCGAAACA AAAAGTTTGA ATTGGGTTTG GAGTTTCCCA ATCTTCCTTA TTATATTGAT	180
257	GGTGATGTTA AATTAACACA GTCTATGGCC ATCATACGTT ATATAGCTGA CAAGCACAAC	240
258	ATGTTGGGTG GTTGTCCAAA AGAGCGTGCA GAGATTTCAG TGCTTGAAGG AGCGGTTTTG	300

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SEQUENCE VERIFICATION REPORT
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Line

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Original Text

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SEQUENCE MISSING ITEM REPORT
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PRIOR APPLICATION DATA More Identifiers Found Than MAX Allowed

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SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/10/008,960

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